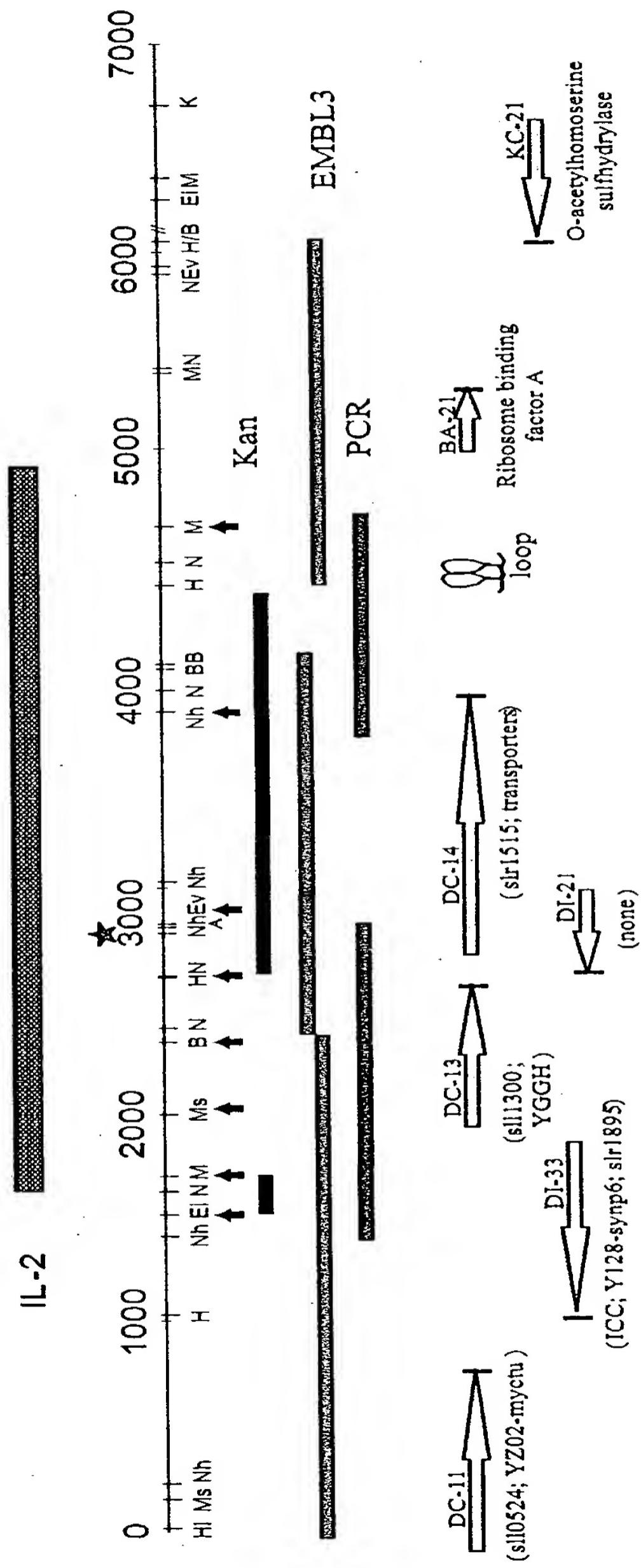


Fig. 1



ICTB	: 120	GGTTGGTCTGAGGCCACTGGT--GGCTTCTGCTGTCGTCTACGGTTCGGCTCCC	177
SLR	: 132	GCCCCACTTGGCATGGTACGGCT-CTAG-TGGCAATAATTATGGGGCTCCC	189

ICTB : 178 TTTGTGCCAGTCCGGCTAGGGTTGGGCGATCGCG-GCCTATTGGGCCCT 236
 ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 |||
 TTCACCTCCACCACTGTTGGCATTTAT-GCTGGCTCTGTGGAGGCCTTTGGCTCT 248
 SLR : 190

Fig. 2

Fig. 2
(Continued)

ICTB : 943 AACTTCCGGATCAATGTCCTGGCTGGCGGTGCTGCAGATGATTCAAGATCGGCCTGGCTG 1002
SLR : 955 ATTTCGGCATCAATGTTGGAAAGGGTAAAGCCATGATCCGAGCCCCCTATCAT 1014

ICTB : 1003 GGATCGGCCGGCAAACCGCCCTTAACCTGGTTTATCCCTCTATAAACAGGGCGGC 1062
SLR : 1015 GGATTCGGCCAGTAAACGAAGCCCTTAACCAAATTATCCTTACTATAACGGGGTAGT 1074

ICTB : 1063 TTACGGCGTTGAGGCCCTACTCCGGCTGGAAAGTCGGGGACTACTG 1122
SLR : 1075 TtCACCGCCCTGAGTCGCCTATTCCATTACCTAGAAATTGGAAACGGGGTAGT 1134

ICTB : 1123 GGCTTGA-CGGCCTTCGGTGGCT-GCTGGTCACGGGGTACGGGGCAGG 1180
SLR : 1135 GGTTTACCTGTATGCTC-TGGCTGGCCGTACCCCTAGGCAAGGGTAGT 1192

ICTB : 1181 TGAGCCGACTGCGGCCGATGCCAATCCC--AAGCCTTGTGATGGCTAGCTGGC 1238
SLR : 1193 TTAACCG-CTGRCGC-CAAACCCCTGGGGAGGCATCTGGATTATGGGGCTTAGC 1250

ICTB : 1239 CGGTTGGCAGGAATGCTGGTCACGGTCTGGTGTACCCGGAAAGC 1298
SLR : 1251 GGCGATCATCGGTTGGCCACGGCATGGTAGATAACAGTCTGGTACCGTCCCCGGT 1310

ICTB : 1299 CAGTACGGCTCTGGCTCTGTATTGG--AGCGATCGCCGAGTTCTGG--CAGC-CCCAA 1353
SLR : 1311 GAGCACTTGTGGTG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTGGCCAGGCCAG 1368

ICTB : 1354 CCTTCCAAAGCAACTCCCTCCAGAAGCCGAGCATTCAGACGAA 1395
SLR : 1369 GCCCGTTGGAGGGCAGTAAAGAA---GAAATGAGGACAAA 1407

Fig. 2
(Continued)

SLR : 5 ISIWRSLMFGGSPSPQEWGRGSVLRRLVGQSWIQASVLUWPHFEALGTLVALIIFIAPPF 64
 + + +W+ +L F + PQ+WG S LHRL G + +W +S L EAIG E+A++ +APP

ICTB : 61 VPSSAIGLGLARIAYWALLSLTDIDLRQATPIHWLVLVLYNGVDALATGLSPVRAARLVG 120
 + + LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G

SLR : 65 TSTTMIGIFMILCGAFWALLTFAADQPGKGLTPHVLVTAWCISAIAVGFSVPVKMAASG 124

ICTB : 121 LAKLTLYLLVFAALARVLRNPRLRSLLFSVVVITSLEPVSVYCLINQWTYGVVEELATWYDRN 180
 LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D

SLR : 125 LAKLTANLCLFLAARLLQNKQWLNRLLVTLVGLLUVSYGLRQQVDGVEQLATWEDPT 184

ICTB : 181 SVADFTSRVYSSYLGNPMLLAAYLVPITTAFSADAIGVWRGHLPKLILIAATGASSICLIUT 240
 S +RVYS+LGNPMLLAAYLVP T S +A+ VWR W PKLL + LCL T

SLR : 185 STLAQATRVSSELGNPMLLAAYLVPMTGLSLSALVWVRRWWPKLLGATWVNLICLFFT 244

ICTB : 241 YSRGGWMLGFVAMIFYWALLGLYWFQPRILPAPWRRMWLFPPVVLGGLVAVLGLEPLRV 300
 SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+

SLR : 245 QSRGGWMLAVLALGATPLALCYFWLWPQLPKFWQRWSLPLAIAVAVVILGGCALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSSNINFRINWVLQMIQDRPWLIGICPGNTAFNLVYPLYQQARFTALSA 360
 R +SIF GREDSSMNINPRINW V MI+ RP +GICPGN AFN +YP Y + RFTALSA

SLR : 305 RAMSIFAGREDSSNINFRINWEGVKAMIRARPPIIGICPGNEAFNQIYPYYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLLIGLTAFAWLLVTAVTAVRQVSRIIRRDRNPQAFWLMASLAGLGMIG 420
 YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L

SLR : 365 YSIYLBILVETGYWGFTCMILWLLAVTLGKGVELVKRCRQTLAPEGIWMGALAALIGLLV 424

ICTB : 421 HGLFD1TVLYRPEASTLWLLCIGAIIASFWQPOPSKOLPPEAEHSDEKM 467
 HG+ DTV YRP STLWLL + +AS W ++ + B+ D+ +

SLR : 425 HGMVDTWVYRPPVSTLWLLVAIVASQWASAQARLEASKEENEDKPL 471

Fig. 3

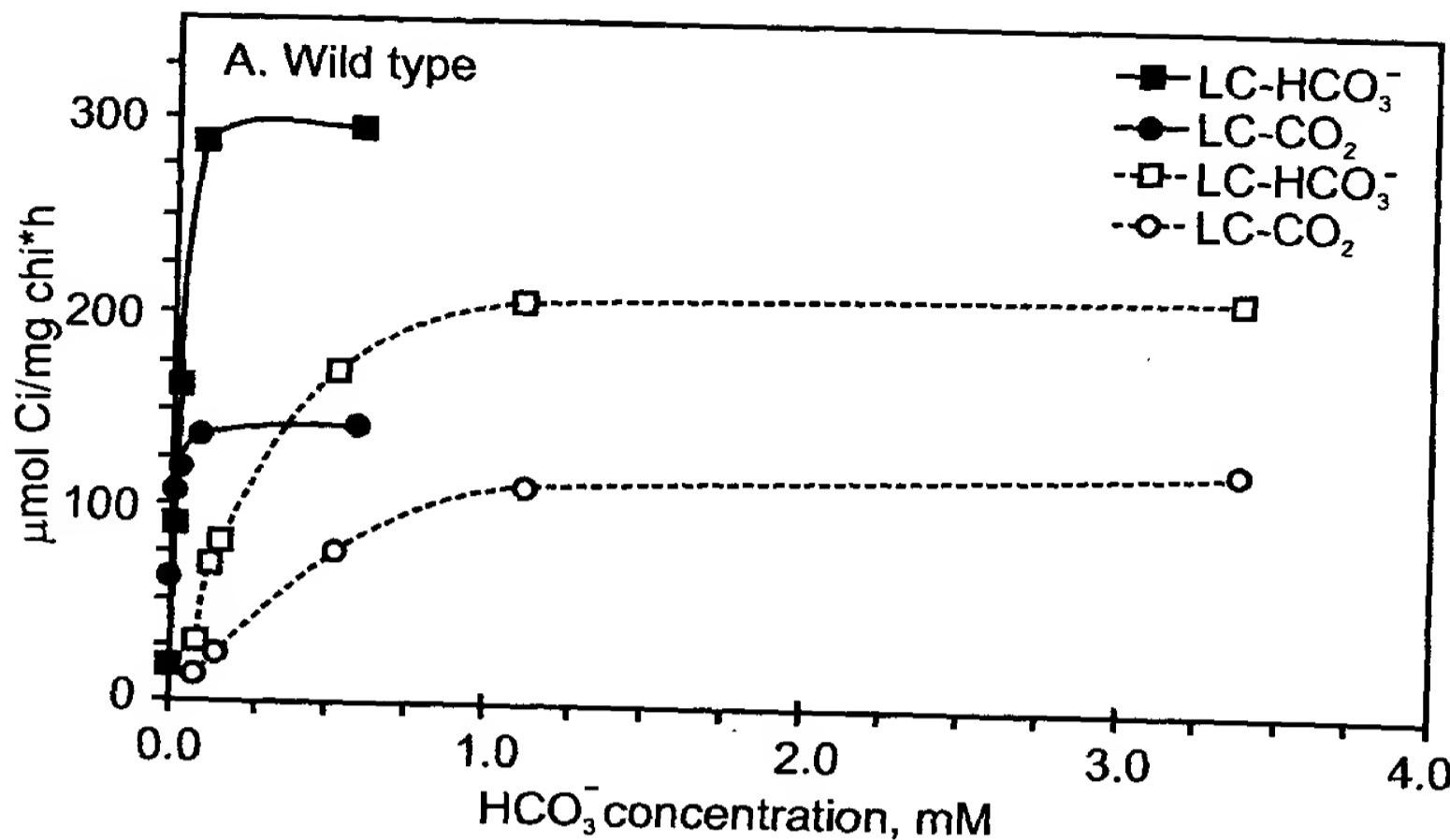


Fig. 4a

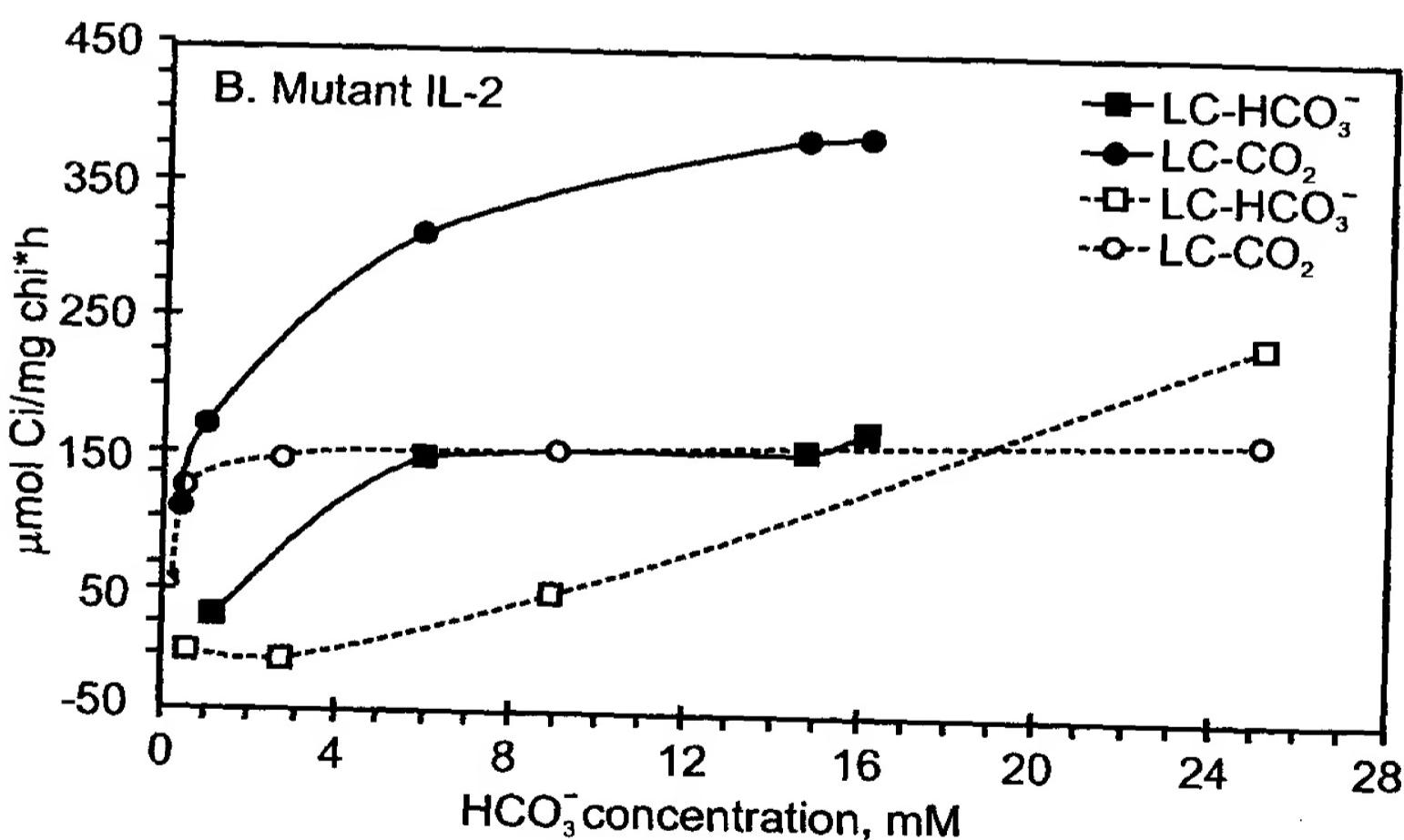


Fig. 4b

Wild type GGGCT-AGCCCGCA-TCCGGCCCTATTGGGCC (SEQ ID NO: 6)
IL-2 ApaI side GGGCT-AG--G-GATCGC-GCCCTATTGGGCC (SEQ ID NO: 7)
IL-2 BamHI side GGGCTCA---GATCGC-GCCCTATTGGGCC (SEQ ID NO: 8)
IctB G L A A I A Y W A L (SEQ ID NO: 9)

Fig. 5

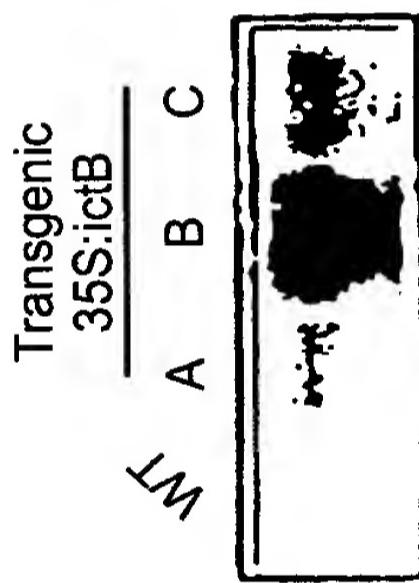


Fig. 6